SEQUENCE LISTING

<110> Merck & Co., Inc.
      Bryan, Janine T.
      Brownlow, Michelle K.
      Schultz, Loren D.
      Jansen, Kathrin U.

<120> OPTIMIZED EXPRESSION OF HPV 45 L1 IN
   YEAST

<130> 21500-PCT

<150> 60/506,812
<151> 2003-09-29

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1533
<212> DNA
<213> Artificial Sequence

<220>
<223> HPV45 L1R

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agattgttga ctgtcggtaa cccatacttc agagtcgtcc catccggtgc tggtaacaag 180
caagctgttc caaaggtctc tgcttaccaa tacagagtct tcagagtcgc tttgccagac 240
ccaaacaagt tcggtttgcc agactctact atctacaacc agaaactca aagattggtc 300
tgggcatgcg tcggtatgga aatcggtaga ggtcaaccat tgggtatcgg tttgtctggt 360
cacccattct acaacaagtt ggacgacacc gaatccgctc acgctgctac tgctgtcatc 420
actcaagacg tcagagacaa cgtctctgtc gactacaagc aaacccaatt gtgtatcttg 480
ggttgtgtcc cagctatcgg tgaacactgg gctaagggta ccttgtgtaa gccagctcaa 540
ttgcaaccag gtgactgtcc accattggaa ttgaagaaca ctatcatcga agacggtgac 600
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gttccattgg acatctgtca atctatctgt aagtacccag actacttgca aatgtccgct 720
gacccatacg gtgactctat gttcttctgt ttgagaagag aacaattgtt cgctagacac 780
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tccgacttgg accaataccc attgggtaga aagttcttgg ttcaagctgg tttgagacgt 1440
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gctaagcgtg tcagaatcag atccaagaag taa   1533

<210> 2
<211> 510
<212> PRT
<213> Human Papillomavirus Type 45

<400> 2
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Ile Phe Tyr His Ala Gly Ser Ser Arg Leu Leu Thr Val Gly Asn Pro
        35              40              45
Tyr Phe Arg Val Val Pro Ser Gly Ala Gly Asn Lys Gln Ala Val Pro
    50              55              60
Lys Val Ser Ala Tyr Gln Tyr Arg Val Phe Arg Val Ala Leu Pro Asp
65              70              75              80
Pro Asn Lys Phe Gly Leu Pro Asp Ser Thr Ile Tyr Asn Pro Glu Thr
                85              90              95
Gln Arg Leu Val Trp Ala Cys Val Gly Met Glu Ile Gly Arg Gly Gln
            100             105             110
Pro Leu Gly Ile Gly Leu Ser Gly His Pro Phe Tyr Asn Lys Leu Asp
        115             120             125
Asp Thr Glu Ser Ala His Ala Ala Thr Ala Val Ile Thr Gln Asp Val
    130             135             140
Arg Asp Asn Val Ser Val Asp Tyr Lys Gln Thr Gln Leu Cys Ile Leu
145             150             155             160
Gly Cys Val Pro Ala Ile Gly Glu His Trp Ala Lys Gly Thr Leu Cys
                165             170             175
Lys Pro Ala Gln Leu Gln Pro Gly Asp Cys Pro Pro Leu Glu Leu Lys
            180             185             190
Asn Thr Ile Ile Glu Asp Gly Asp Met Val Asp Thr Gly Tyr Gly Ala
            195             200             205
Met Asp Phe Ser Thr Leu Gln Asp Thr Lys Cys Glu Val Pro Leu Asp
    210             215             220
Ile Cys Gln Ser Ile Cys Lys Tyr Pro Asp Tyr Leu Gln Met Ser Ala
225             230             235             240
Asp Pro Tyr Gly Asp Ser Met Phe Phe Cys Leu Arg Arg Glu Gln Leu
                245             250             255
Phe Ala Arg His Phe Trp Asn Arg Ala Gly Val Met Gly Asp Thr Val
            260             265             270
Pro Thr Asp Leu Tyr Ile Lys Gly Thr Ser Ala Asn Met Arg Glu Thr
        275             280             285
Pro Gly Ser Cys Val Tyr Ser Pro Ser Pro Ser Gly Ser Ile Thr Thr
    290             295             300
Ser Asp Ser Gln Leu Phe Asn Lys Pro Tyr Trp Leu His Lys Ala Gln
305             310             315             320
Gly His Asn Asn Gly Ile Cys Trp His Asn Gln Leu Phe Val Thr Val
            325             330             335
Val Asp Thr Thr Arg Ser Thr Asn Leu Thr Leu Cys Ala Ser Thr Gln
        340             345             350
Asn Pro Val Pro Asn Thr Tyr Asp Pro Thr Lys Phe Lys His Tyr Ser
        355             360             365
Arg His Val Glu Glu Tyr Asp Leu Gln Phe Ile Phe Gln Leu Cys Thr
    370             375             380
Ile Thr Leu Thr Ala Glu Val Met Ser Tyr Ile His Ser Met Asn Ser
385             390             395             400
Ser Ile Leu Glu Asn Trp Asn Phe Gly Val Pro Pro Pro Pro Thr Thr
            405             410             415
Ser Leu Val Asp Thr Tyr Arg Phe Val Gln Ser Val Ala Val Thr Cys
            420             425             430
Gln Lys Asp Thr Thr Pro Pro Glu Lys Gln Asp Pro Tyr Asp Lys Leu
        435             440             445
Lys Phe Trp Thr Val Asp Leu Lys Glu Lys Phe Ser Ser Asp Leu Asp
    450             455             460
Gln Tyr Pro Leu Gly Arg Lys Phe Leu Val Gln Ala Gly Leu Arg Arg
465             470             475             480
Arg Pro Thr Ile Gly Pro Arg Lys Arg Pro Ala Ala Ser Thr Ser Thr
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Ala Ser Arg Pro Ala Lys Arg Val Arg Ile Arg Ser Lys Lys
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<210> 3
<211> 1533
<212> DNA
<213> Human Papillomavirus Type 45

<400> 3
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cgattattaa ctgtaggcaa tccatatttt aggggttgtac ctagtggtgc aggtaataaa 180
caggctgttc ctaaggtatc cgcatatcag tataggggtgt ttagagtagc tttgcccgat 240
cctaataaat ttggattacc tgattctact atatataatc ctgaaacaca acgtttggtt 300
tgggcatgtg taggtatgga aattggtcgt gggcagcctt taggtattgg cctaagtggc 360
catccatttt ataataaatt ggatgataca gaaagtgctc atgcagctac agctgttatt 420
acgcaggatg ttagggataa tgtgtcagtt gattataagc aaacacagct gtgtatttta 480
ggttgtgtac ctgctattgg tgagcactgg gccaagggca cactttgtaa acctgcacaa 540
ttgcaacctg gtgactgtcc tcctttggaa cttaaaaaca ccattattga ggatggtgat 600
atggtggata caggttatgg ggcaatggat tttagtacat tgcaggatac aaagtgcgag 660
gttccattag acatttgtca atccatctgt aaatatccag attatttgca aatgtctgct 720
gatccctatg gggattctat gtttttttgc ctacgccgtg aacaactgtt tgcaagacat 780
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tctattacta cttctgattc tcaattattt aataagccat attggttaca taaggcccag 960
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cctactaagt ttaagcacta tagtagacat gtgggaggaat atgatttaca gtttattttt 1140
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aagcaggatc catatgataa attaaagttt tggactgttg acctaaagga aaaattttcc 1380
tccgatttgg atcaatatcc ccttggtcga aagtttttag ttcaggctgg gttacgtcgt 1440
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<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 4
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<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 5
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<210> 6
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

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<210> 7
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 7
gacagatctt atttttact acgtatacgt acacg                               35

<210> 8
<211> 1533
<212> DNA
<213> Artificial Sequence

<220>
<223> HPV45 L1R - Antisense

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ccaacacagg gtcgatagcc acttgtgacc cgattcccat ggaacacatt cggtcgagtt 540
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aagaccttgt ctcgaccaca gtacccactg tgacaaggtt gactgaacat gtagttccca 840
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